

Figure 1A. Nucleic acid encoding human Cloaked-2 polypeptide with signal peptide (SEQ ID NO:1)

1 TACTGGAAGGTGGCGTGCCCTCCTCTGGCTGGTACC**ATG**CAGCTCCCACT  
 51 GGCCTGTGTCTCGTCTGCCTGCTGGTACACACAGCCTTCCGTGTAGTGG  
 101 AGGGCCAGGGGTGGCAGGCGTTCAAGAATGATGCCACGGAATCATCCCC  
 151 GAGCTCGGAGAGTACCCCGAGCCTCCACCGAGCTGGAGAACACAAGAC  
 201 CATGAACCGGGCGGAGAACGGAGGGCGGCCTCCCCACCACCCTTTGAGA  
 251 CCAAAGACGTGTCCGAGTACAGCTGCCGCGAGCTGCACTTCACCCGCTAC  
 301 GTGACCGATGGGCGGTGCCGCAGCGCCAAGCCGGTCACCGAGCTGGTGTG  
 351 CTCGGCCAGTGGCGCCCGCGGCCTGCTGCCCAACGCCATCGGCCGCG  
 401 GCAAGTGGTGGCGACCTAGTGGGCGCGACTTCCGCTGCATCCCCGACCGC  
 451 TACCGCGCGCAGCGCGTGCAGCTGCTGTGTCCCGGTGGTGAGGCGCGCG  
 501 CGCGCGCAAGGTGCGCCTGGTGGCCTCGTGCAAGTGCAAGCGCCTCACCC  
 551 GCTTCCACAACCAGTCCGAGCTCAAGGACTTCGGGACCGAGGCGCTCGG  
 601 CCGCAGAAAGGCCGGAAGCCGCGGCCCGCGCCCGAGCGCCAAAGCCAA  
 651 CCAGGCCGAGCTGGAGAACGCCTAC**TAG**AGCCCCCGCGCCCCCTCCCCA  
 701 CCGCGGGCGCCCCGGCCCTGAACCCGCGCCCCACATTCTGTCTCTGC  
 751 GCGTGGTTT

B. Human Cloaked-2 polypeptide most likely mature form (SEQ ID NO:2)

1 QGWQAFKNDATETIIPELGEYPEPPPELENNKTMNRAENGGRPPHHPFETK  
 51 DVSEYS**C**RELHFTRYVTDGP**C**RSAKPVTELV**CSGQ**CGPARLLPNAIGRGK  
 101 WWRPSGPDFR**C**IPDRYRAQRVQLL**C**PGGEAPRARKVRLVAS**CK**CKRLTRF  
 151 HNQSELKDFGTEAARPQKGRKPRPRARSAKANQAELENAY

C. Human Cloaked-2 polypeptide with signal peptide (SEQ ID NO:5)

1 MQLPLALCLVCLLVHTAFRVVEGQGWQAFKNDATETIIPELGEYPEPPPEL  
 51 ENNKTMNRAENGGRPPHHPFETKDVSEYSCRELHFTRYVTDGPCRSAKPV  
 101 TELVCSGQCGPARLLPNAIGRGKWWWRPSGPDFRCIPDRYRAQRVQLLCPG  
 151 GEAPRARKVRLVASCKCKRLTRFHNQSELKDFGTEAARPQKGRKPRPRAR  
 201 SAKANQAELENAY

T0630-42980

## Figure 2

### A. Nucleic acid encoding mouse Cloaked-2 polypeptide with signal peptide (SEQ ID NO:3)

```

1  ATGCAGCCCTCACTAGCCCCGTGCCTCATCTGCCTACTTGTGCACGCTGC
51  CTTCTGTGCTGTGGAGGGCCAGGGGTGGCAAGCCTTCAGGAATGATGCCA
101 CAGAGGTCATCCCAGGGCTTGGAGAGTACCCCGAGCCTCCTCCTGAGAAC
151 AACCAGACCATGAACCGGGCGGAGAAATGGAGGCAGACCTCCCCACCATCC
201 CTATGACGCCAAAGATGTGTCCGAGTACAGCTGCCGCGAGCTGCACTACA
251 CCCGCTTCCTGACAGACGGCCCATGCCGCAGCGCCAAGCCGGTCACCGAG
301 TTGGTGTGCTCCGGCCAGTGC GGCCCCCGCGCGGCTGCTGCCCAACGCCAT
351 CGGGCGCGTGAAGTGGTGGCGCCCCGAACGGACCGGATTTCCGCTGCATCC
401 CGGATCGCTACCGCGCGCAGCGGGTGCAGCTGCTGTGCCCCGGGGGCGCG
451 GCGCCGCGCTCGCGCAAGGTGCGTCTGGTGGCCTCGTGCAAGTGCAAGCG
501 CCTACCCGCTTCCACAACCAAGTCGGAGCTCAAGGACTTCGGGCCGGAGA
551 CCGCGCGGCCCGAGAAGGGTCGCAAGCCGCGGCCCGCGCCCGGGGAGCC
601 AAAGCCAACCAGGCGGAGCTGGAGAACGCCTACTAG

```

### B. Mouse Cloaked-2 polypeptide most likely mature form (SEQ ID NO:4)

```

1  QGWQAFRNDATEVIPGLGEYPEPPPENNTMNRAENGGRPPHHHPYDAKDV
51  SEYSCRELHYTRFLTDGPCRSAPVTELVCSGQCGPARLLPNAIGRVKWW
101 RPNGPDFRCIPDRYRAQRVQLLCPGGAAPRSRKVRLVASCKCKRLTRFHN
151 QSELKDFGPETARPQKGRKPRPGARGAKANQAELENAY

```

### C. Mouse Cloaked-2 polypeptide with signal peptide (SEQ ID NO:6)

```

1  MQPSLAPCLICLLVHAAFCAVEGQGWQAFRNDATEVIPGLGEYPEPPPEN
51  NQTMNRAENGGRPPHHHPYDAKDVSEYSCRELHYTRFLTDGPCRSAPVTE
101 LVCSGQCGPARLLPNAIGRVKWWRPNGPDFRCIPDRYRAQRVQLLCPGGA
151 APRSRKVRLVASCKCKRLTRFHNQSELKDFGPETARPQKGRKPRPGARGA
201 KANQAELENAY

```

Figure 3

GAP of: Human Cloaked-2 check: 5775 from: 1 to: 213  
 to: Mouse Cloaked-2 check: 9489 from: 1 to: 211

Symbol comparison table:  
 /GCGDISK/gcg10/gcgcore/data/rundata/blosum62.cmp  
 CompCheck: 6430

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	1028	Length:	213
Ratio:	4.872	Gaps:	1
Percent Similarity:	91.469	Percent Identity:	88.152

Match display thresholds for the alignment(s):

```

| = IDENTITY
: = 2
. = 1

```

Human Cloaked-2 (SEQ ID NO: 5) x  
Mouse Cloaked-2 (SEQ ID NO: 6)

```

1  MQLPLALCLVCLLVHTAFRVVEGQGWQAFKNDATETIIPELGEYPEPPPEL 50
   ||  ||  ||:|||||  ||  |||||||||:||||:|  |||||||||
1  MQPSLAPCLICLLVHAAFCAVEGQGWQAFRNDATEVIPGLGEYPEPPP.. 48

51  ENNKTMNRAENGGRPPHHPFETKDVSEYSCRELHFTRYVTDGPCRSAKPV 100
   |||.|||||||||||||:|  |||||||||||:|:|.|||||||||
49  ENNQTMNRAENGGRPPHHPYDAKDVSEYSCRELHYTRFLTGDGPCRSAKPV 98

101 TELVCSGQCGPARLLPNAIGRGKWWRPSPGPDFRCIPDRYRAQRVQLLCPG 150
     |||||||||||||||  |||.|||||||||
99  TELVCSGQCGPARLLPNAIGRVKWWRPNGPDFRCIPDRYRAQRVQLLCPG 148

151 GEAPRARKVRLVASCKCKRLTRFHNQSELKDFGTEAAPQKGRKPRPRAR 200
   | |||.|||||||||||||  |||||||||||
149 GAAPRSRKVRLVASCKCKRLTRFHNQSELKDFGPETARPQKGRKPRPGAR 198

201 SAKANQAELENAY 213
     |||||||||||
199 GAKANQAELENAY 211

```

## Figure 4

```
GAP of: Human Cloaked-1  check: 1888  from: 1  to: 183
      to: Human Cloaked-2  check: 185  from: 1  to: 190
```

```
Symbol comparison table:
/GCGDISK/gcgl0/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430
```

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	335	Length:	196
Ratio:	1.831	Gaps:	6
Percent Similarity:	52.542	Percent Identity:	42.938

```
Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1
```

$$\frac{\text{Human Cloaked-1 (SEQ ID NO: 25)} \times \text{Human Cloaked-2 (SEQ ID NO: 2)}}{\text{Human Cloaked-2 (SEQ ID NO: 2)}}$$

```

1 .....FKNDATEILYSHVVKP.VPAHPSSNSTLNQARNGGRHFSNTGLDR 44
      |||||: | | | | | | | | | | | | | | | | | | | | | |
1 QGWQAFKNDATEIIPELGEYPEPPPELENNKTMNRAENGGRP.PHHPFET 49
      . . . . .
45 NTRVQVGCRELRSTKYISDGQC+TSISPLKELVCAGECLPLPVLPNWIGGG 94
      : |||| | : | : . || | | | . |||| | : | | | . ||| || |
50 KDVSEYSCRELHFTRYVTDGPGCRSAKPVTELVCSGQCGPARLLPNAIGRG 99
      . . . . .
95 YGTKYWSRRSSQEWRCVNDKTRTQRIQLQCQDG.STRTYKITVVTACKCK 143
      | : | | | : . || : | : | | : || | | | . | | : . | . ||||
100 ...KWW.RPSGPDPRCIPDRYRAQRVQLLCPGGEAPRARKVRLVASCKCK 145
      . . . . .
144 RYTRQHNESSHNPFESMSPAKVPQHHRRERKRASKSSKHSMS..... 183
      | | | | : | | | | : | : | | | : | . . .
146 RLTRFHNQSELKDFGTEAARPQKGRKPRPRA.RSAKANQAELENAY 190

```